

Phytophthora genotyping, Oomycete metabarcoding, novel genomic tools

Niklaus J. Grunwald

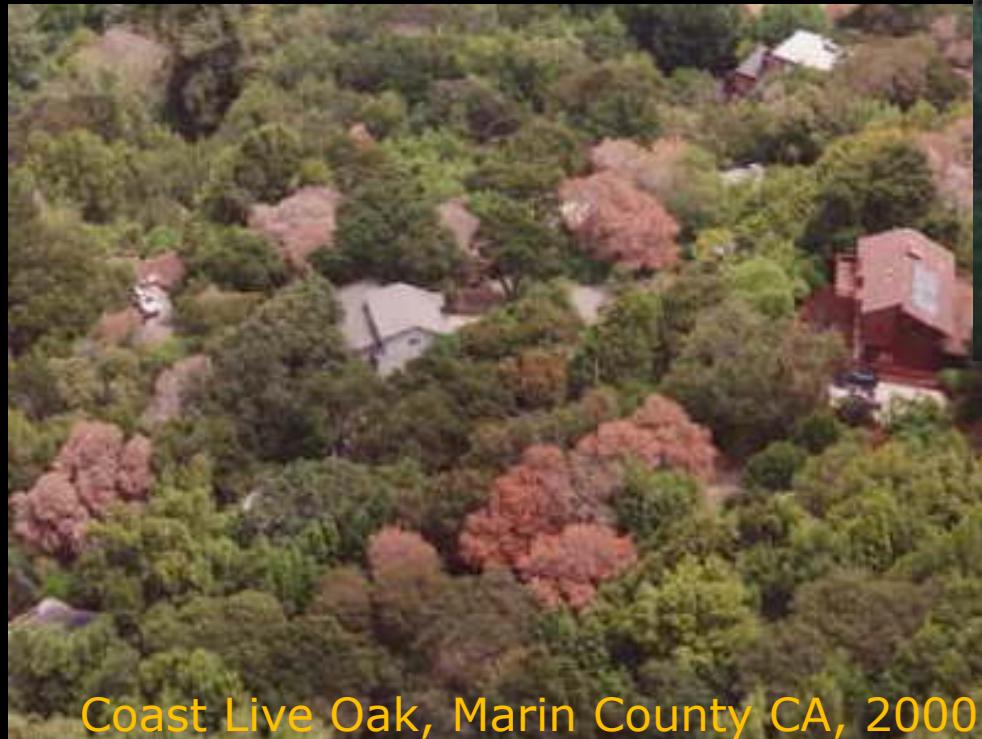
Horticultural Crops Research Lab, USDA ARS, Corvallis,
OR, USA

Recent and ongoing collaborations

- Richard Hamelin, UBC:
 - Resequencing of *Phytophthora ramorum* genomes
 - Extensive ROH
- Richard Bélanger, U laval
 - *P. sojae* population genomics
- Hai Nguyen, AAFC:
 - Development of rps10 locus for metabarcoding

Phytophthora ramorum

Sudden oak death



Coast Live Oak, Marin County CA, 2000



Tan oak, Marin County CA, 2000

Photos courtesy Marin County Fire Dept.

Phytophthora ramorum

Letter to the Editor

e-Xtra*

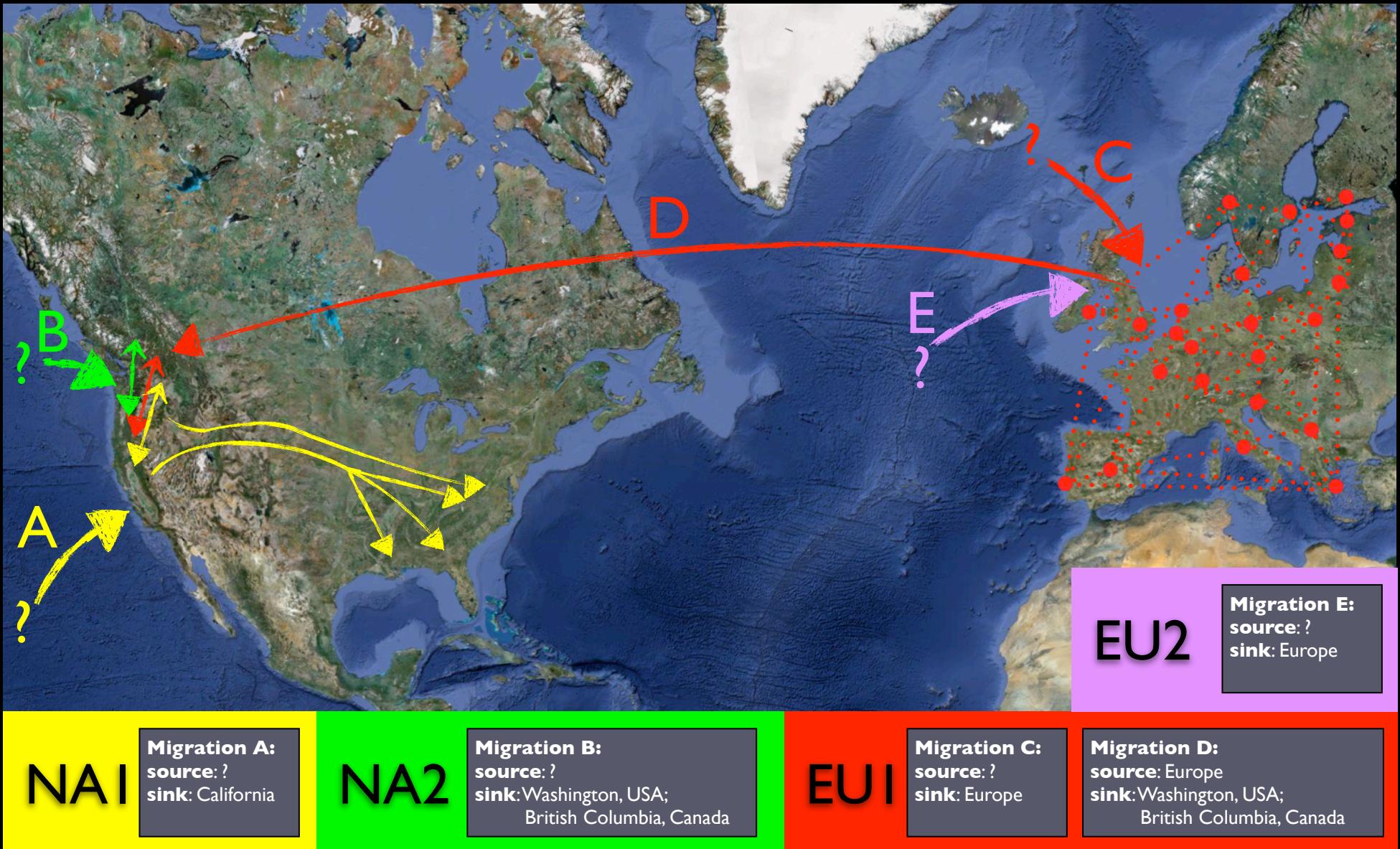
Standardizing the Nomenclature for Clonal Lineages of the Sudden Oak Death Pathogen, *Phytophthora ramorum*

Niklaus J. Grünwald, Erica M. Goss, Kelly Ivors, Matteo Garbelotto, Frank N. Martin, Simone Prospero, Everett Hansen, Peter J. M. Bonants, Richard C. Hamelin, Gary Chastagner, Sabine Werres, David M. Rizzo, Gloria Abad, Paul Beales, Guillaume J. Bilodeau, Cheryl L. Blomquist, Clive Brasier, Stephan C. Brière, Anne Chandelier, Jennifer M. Davidson, Sandra Denman, Marianne Elliott, Susan J. Frankel, Ellen M. Goheen, Hans de Gruyter, Kurt Heungens, Delano James, Alan Kanaskie, Michael G. McWilliams, Willem Man in 't Veld, Eduardo Moralejo, Nancy K. Osterbauer, Mary E. Palm, Jennifer L. Parke, Ana Maria Perez Sierra, Simon F. Shamoun, Nina Shishkoff, Paul W. Tooley, Anna Maria Vettraino, Joan Webber, and Timothy L. Widmer

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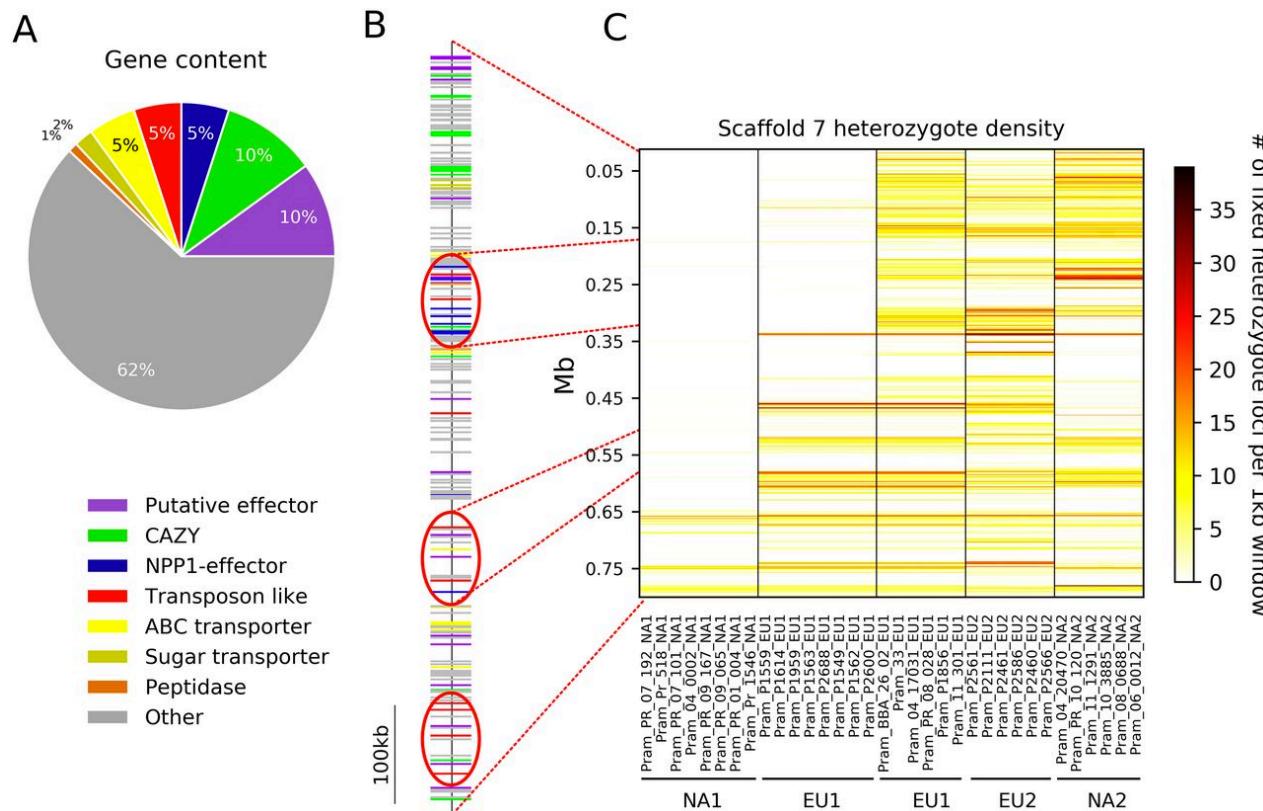
Accepted for publication 8 March 2009.

5 migrations



Trends in Microbiology (2012); Van Poucke *et al.* 2012

Phytophthora ramorum genetics



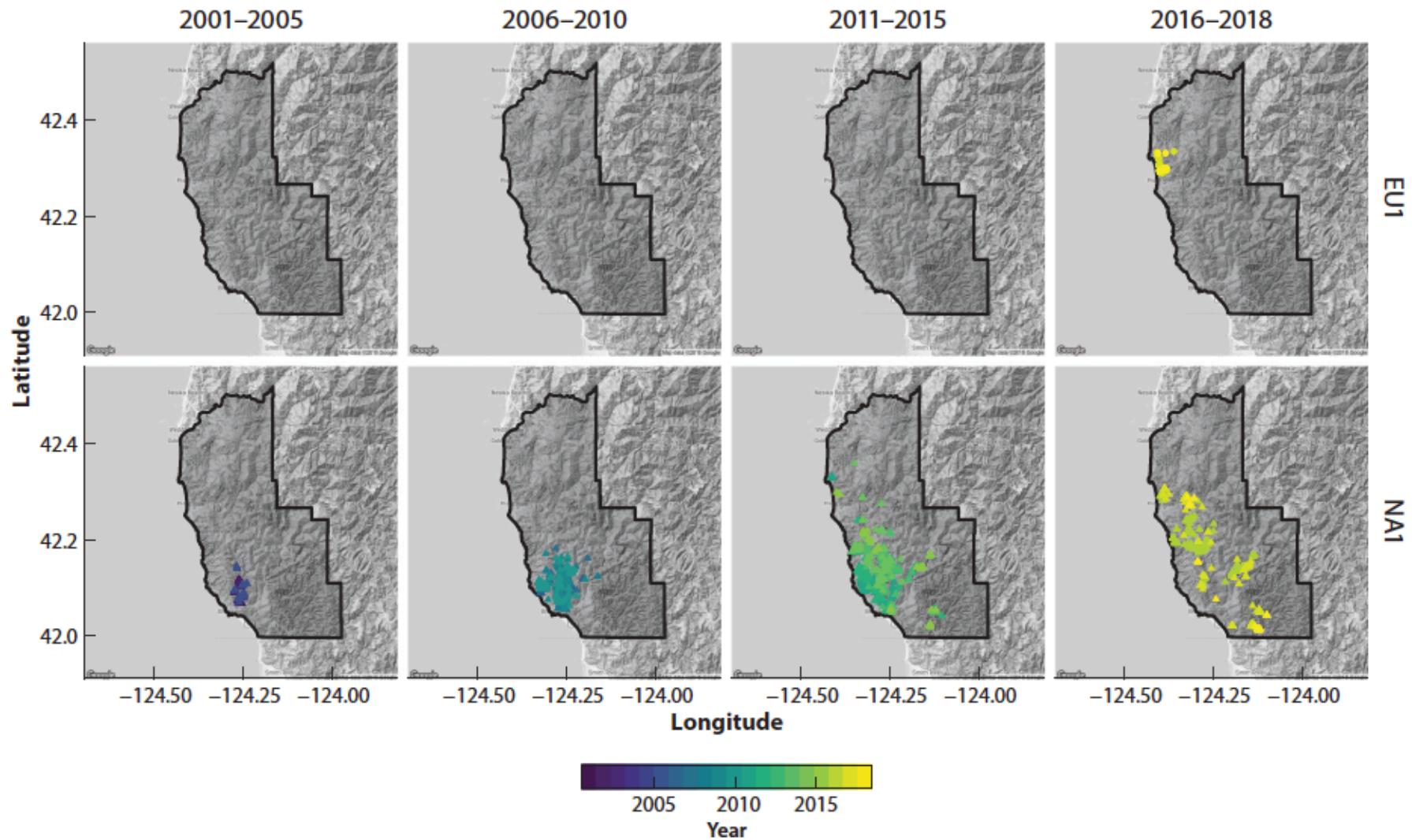


Figure 12

Spatial and temporal dynamics of the emergence of the sudden oak death pathogen in forests in Curry County, Oregon, from 2001 to the present. The EU1 lineage is shown in the top row and NA1 lineage at the bottom (47, 60, 61).

Annual Review of Phytopathology

Ecology and Evolution of the
Sudden Oak Death Pathogen
Phytophthora ramorum

Niklaus J. Grünwald,¹ Jared M. LeBoldus,^{2,3}
and Richard C. Hamelin^{4,5}

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Sudden oak death confirmed in Ohio; report possible infected plants

From the Ohio Department of Agriculture, Office of Communication Jul 16, 2019 



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CULTURE

Pathogen That Causes Tree-Killing Disease Found In Illinois

Alex Ruppenthal | July 2, 2019 3:54 pm



Leaves on a tree affected with sudden oak death (Courtesy California Oak Mortality Task Force)

The pathogen behind a plant disease that has killed large numbers of oak trees and native plant species in California, Oregon and Europe has now been identified in Illinois.



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West Virginia confirms infected rhododendron shipments

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Phenomorum symptoms on a rhododendron. (Joseph OBrien photo, USDA Forest Service)

ARLESTON, W.Va. — The West Virginia Department of Agriculture has confirmed that



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NA2 clonal lineage



Leaves on a tree affected with sudden oak death (Courtesy California Oak Mortality Task Force)

The pathogen behind a plant disease that has killed large numbers of oak trees and native plant species in California, Oregon and Europe has now been identified in Illinois.

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symptoms on a rhododendron. (Joseph OBrien photo, USDA Forest Service)

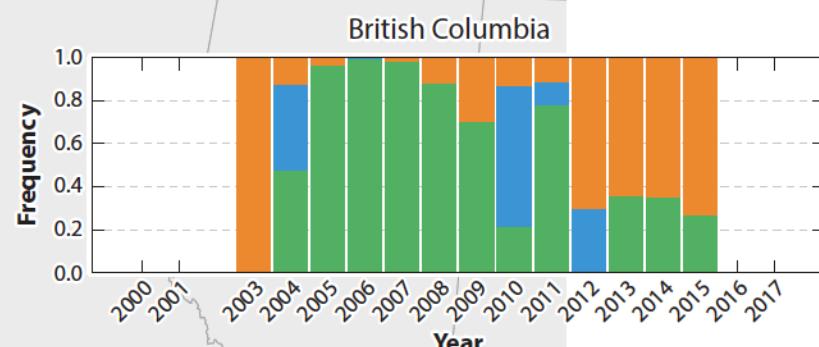
ARLESTON, W.Va. — The West Virginia Department of Agriculture has confirmed that

Sudden oak death: possible infection

From the Ohio Department of Agriculture

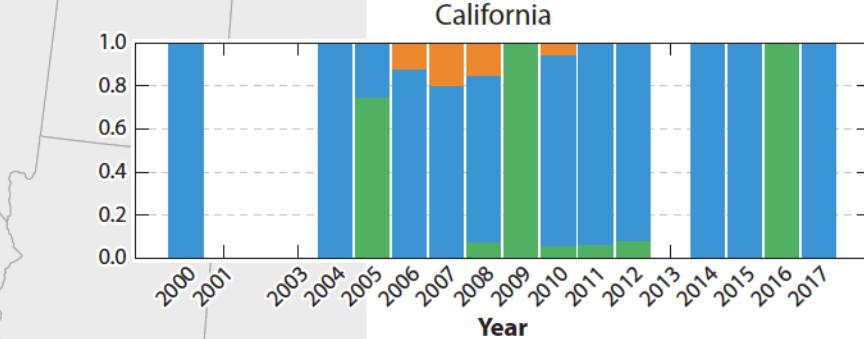
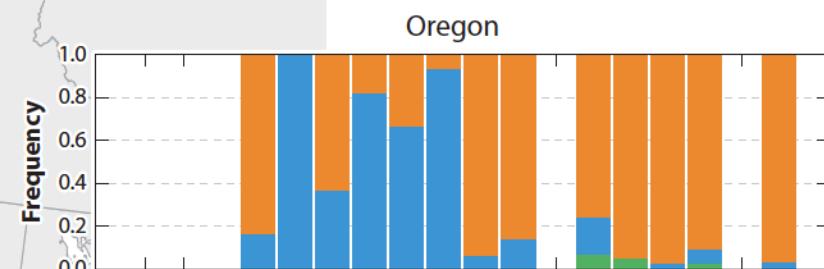
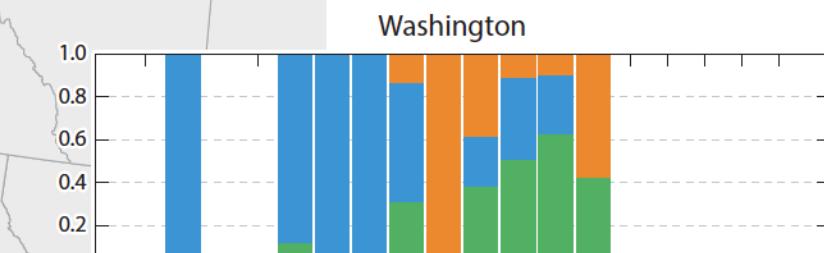


Submitted Photo



Lineage

- EU1
- NA1
- NA2



Annual Review of Phytopathology

Ecology and Evolution of the Sudden Oak Death Pathogen *Phytophthora ramorum*

Niklaus J. Grünwald,¹ Jared M. LeBoldus,^{2,3}
and Richard C. Hamelin^{4,5}



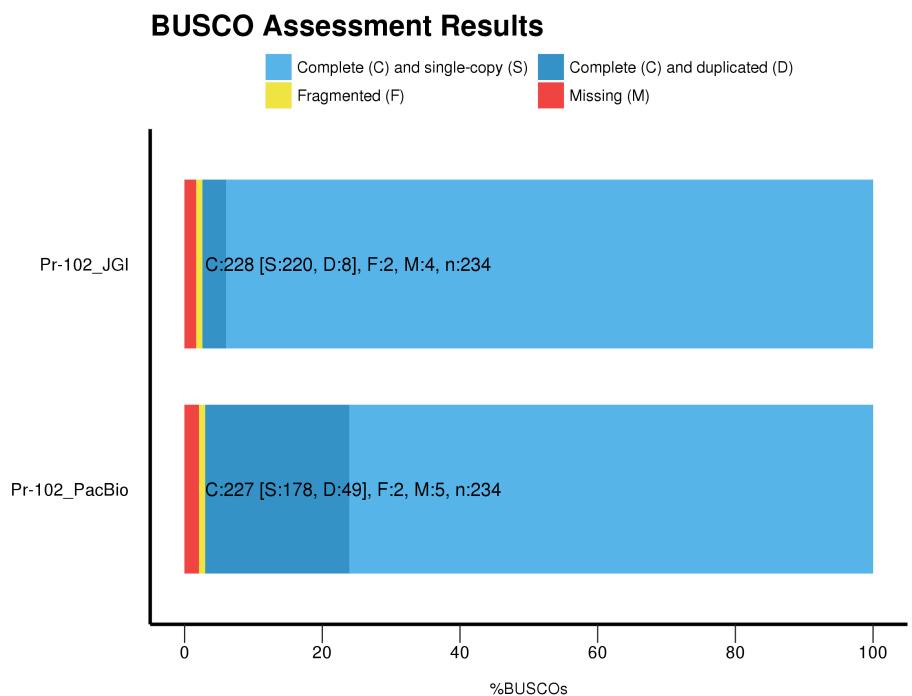
Service)

HAROLD'S EQUIPMENT INC.

Genome sequencing

- PacBio genomes of Pr-102, EU1 and 3 Asian samples
 - New, improved reference genome; shared with UBC
- Resequencing using HiSeq for population genomic and comparative genomic work

Genome	PR102 (JGI)	PR102 (PacBio)
Contigs	2576	137
Genome size	67Mb	75Mb
N50	350kb	1.2 Mb



New *rps10* oomycete metabarcode

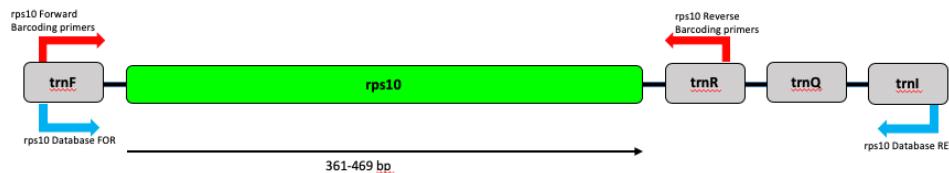


- **Frank N. Martin¹, Felipe Albornoz^{*2}, Zachary S. L. Foster^{*2}, Valerie J. Fieland², Meredith M. Larsen³, F. Andrew Jones³, Brett M. Tyler³, Hai Nguyen⁴, Hermann Voglmayr⁵, Treena Burgess⁶, Jo Anne Crouch⁷, and Niklaus J. Grünwald³**

¹Crop Improvement and Protection Research, Agricultural Research Service, USDA, Salinas, CA, 93905; ² Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331; ³ Horticultural Crops Research Unit, Agricultural Research Service, USDA, Corvallis, OR, 97330; ⁴ Agriculture and Agri-Food Canada, Ottawa, Canada K1A OC6; ⁵Institute of Forest Entomology, Forest Pathology and Forest Protection, Dept. of Forest and Soil Sciences, BOKU-University of Natural Resources and Life Sciences, Franz Schwackhöfer Haus, Peter-Jordan-Straße 82/I, 1190 Vienna, Austria; ⁶Centre for Phytophthora Science and Management, Murdoch University, Murdoch, Western Australia, Australia. 6150; ⁷USDA-ARS, 10300 Baltimore Ave. Bldg 10A, Beltsville, MD 20705

rps10 mtDNA locus

- Amplicon of 361-469bp for MiSeq
- Validate reference database
- Website for download of *rps10* DB
- Submissions welcome

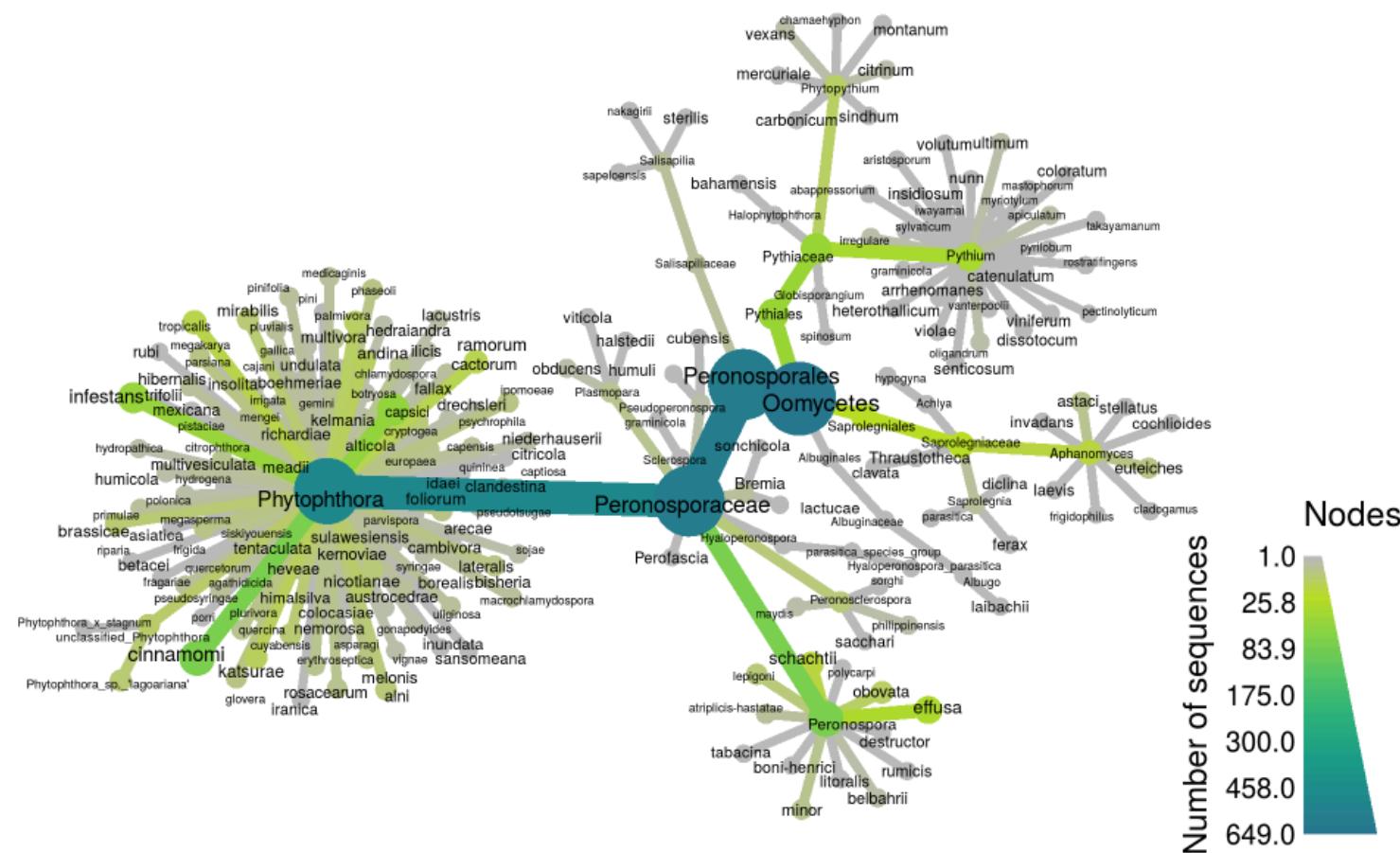


Genus	Number of species	Number of sequences
<i>Phytophthora</i>	110	492
<i>Pythium</i>	27	31
<i>Peronospora</i>	13	73
<i>Aphanomyces</i>	8	15
<i>Phytophytium</i>	7	9
<i>Peronosclerospora</i>	4	6
<i>Plasmopara</i>	3	4
<i>Salisapilia</i>	3	3
<i>Saprolegnia</i>	3	3
<i>Bremia</i>	2	3
<i>Hyaloperonospora</i>	2	1
<i>Pseudoperonospora</i>	2	2
<i>Achlya</i>	1	1
<i>Albugo</i>	1	1
<i>Halophytophthora</i>	1	1
<i>Globisporangium</i>	1	1
<i>Sclerospora</i>	1	1
<i>Thraustotheca</i>	1	1
Total	190	648

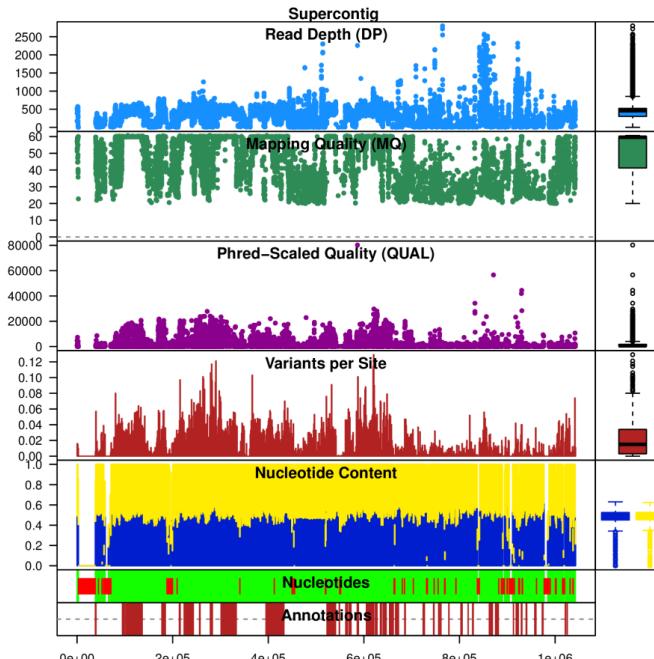
Rps10, a molecular barcode with high sensitivity and specificity for oomycetes

This website is an early release. Please use with caution and get in touch with us if you find an issue.

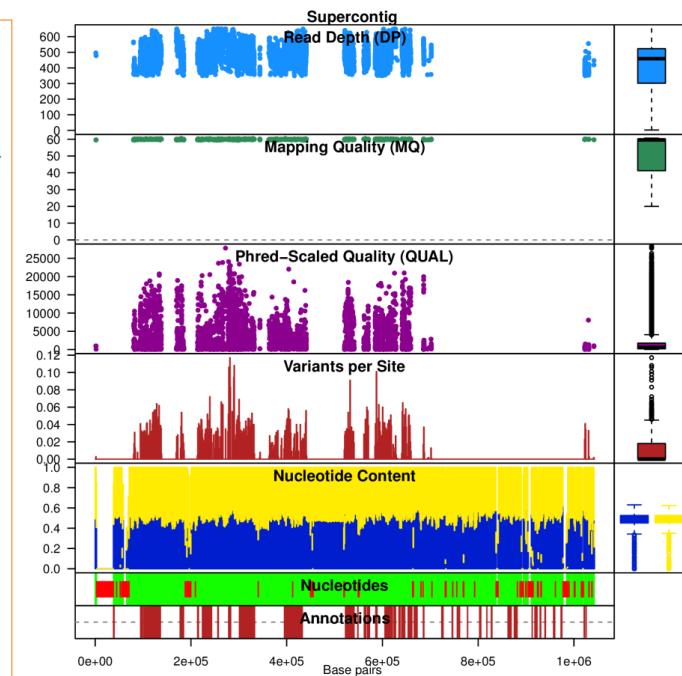
OomyceteDB provides quality-controlled, aligned and annotated Oomycete *rps10* sequences. *rps10* is a mitochondrial locus chosen as a molecular barcode suitable for metabarcoding or amplicon sequencing specific to the Oomycetes. The curated database can be downloaded or queried using BLAST (for any release). We invite all members of the oomycete community to contribute sequences for new Oomycete species. We will include any new taxon with a GenBank accession you share with us. The following heat-tree shows the species currently represented in the database:



VcfR: an R package to manipulate and visualize VCF format data



```
# Load packages.  
library(vcfR)  
library(pinfsc50)  
  
# Locate files.  
vcf_file <- system.file("extdata", "pinf_sc50.vcf.gz",  
                        package = "pinfsc50")  
dna_file <- system.file("extdata", "pinf_sc50.fasta",  
                        package = "pinfsc50")  
gff_file <- system.file("extdata", "pinf_sc50.gff",  
                        package = "pinfsc50")  
  
# Input files.  
vcf <- read.vcfR(vcf_file, verbose = FALSE)  
dna <- ape::read.dna(dna_file, format = "fasta")  
gff <- read.table(gff_file, sep="\t", quote="")  
  
# Create and process chromR object.  
chrom <- create.chromR(name="Supercontig",  
                        vcf=vcf, seq=dna,  
                        ann=gff)  
chrom <- masker(chrom, min_QUAL=0, min_DP=350,  
                  max_DP=650, min_MQ=59.5,  
                  max_MQ=60.5)  
chrom <- proc.chromR(chrom)  
  
# Plot chromR object.  
chromqc(chrom)
```



Special Issue: Population Genomics with R

VcfR: a package to manipulate and visualize variant call format data in R

Brian J. Knaus, Niklaus J. Grünwald

First published: 12 July 2016 Full publication history

DOI: 10.1111/1755-0998.12549 View/save citation



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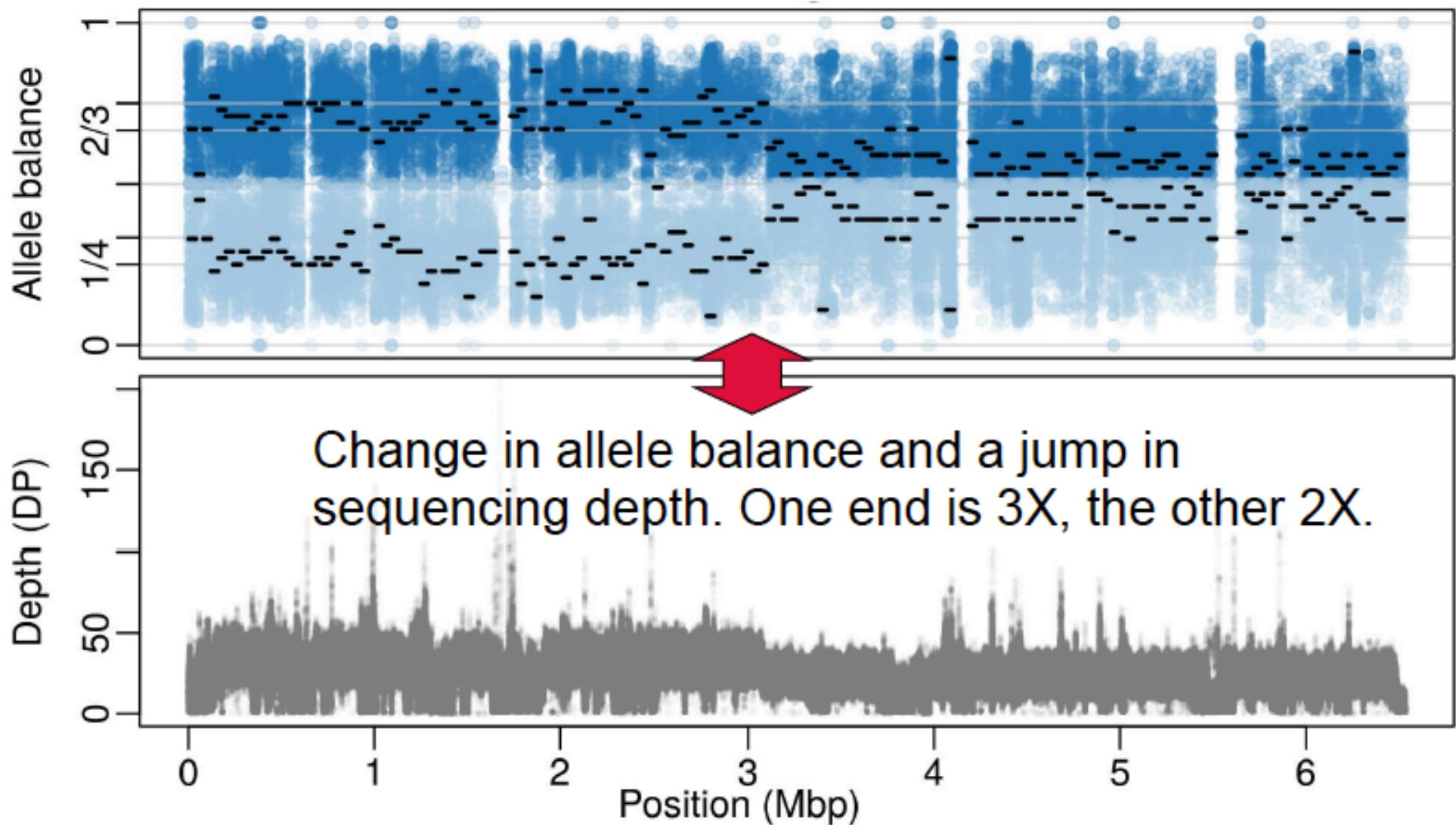
New Results

VcfR: an R package to manipulate and visualize VCF format data

Brian J. Knaus, Niklaus J. Grünwald

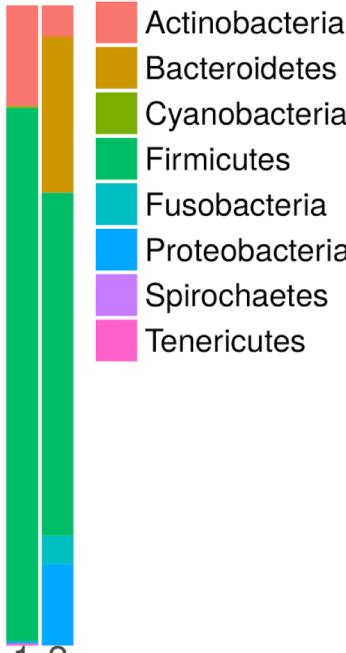
doi: <http://dx.doi.org/10.1101/041277>

EU1: P2346 contig0001



Metacoder: An R package for visualization and manipulation of community taxonomic diversity data

- Stacked bar/pie charts commonly used to plot community composition
- Color representing taxa limits number of taxa that can be plotted



RESEARCH ARTICLE

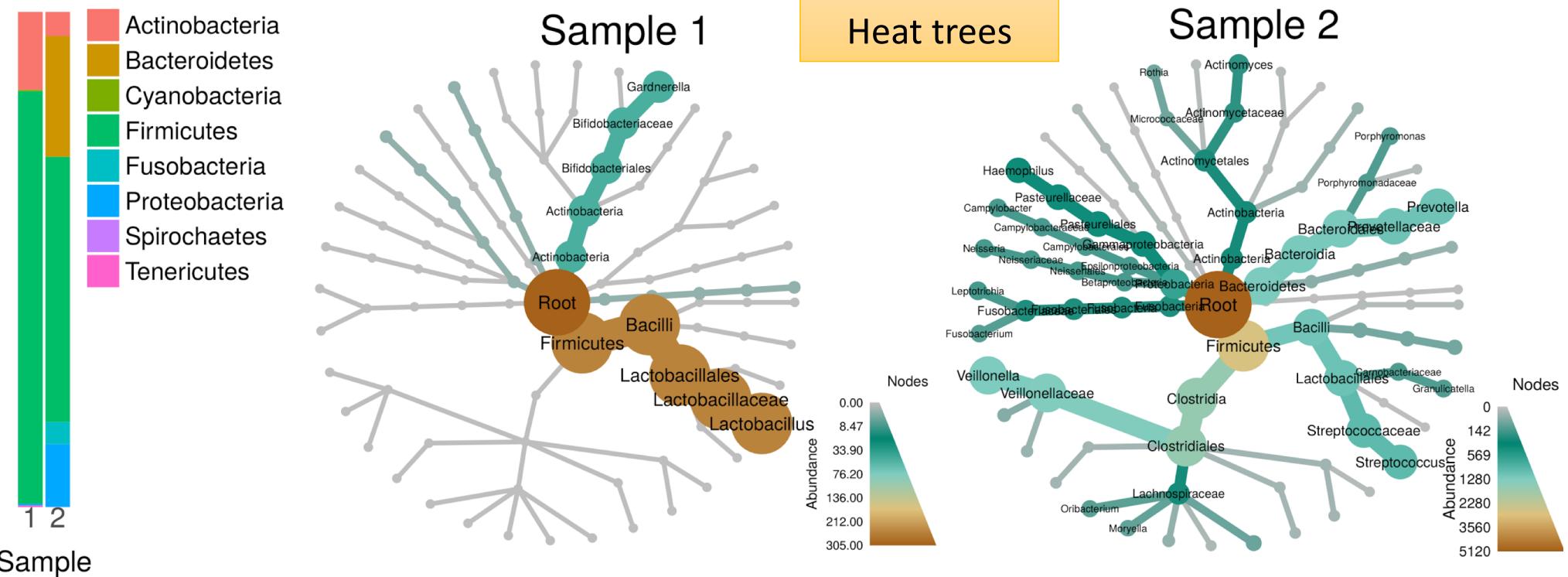
Metacoder: An R package for visualization and manipulation of community taxonomic diversity data

Zachary S. L. Foster¹, Thomas J. Sharpton^{2,3,4}, Niklaus J. Grünwald^{5*}



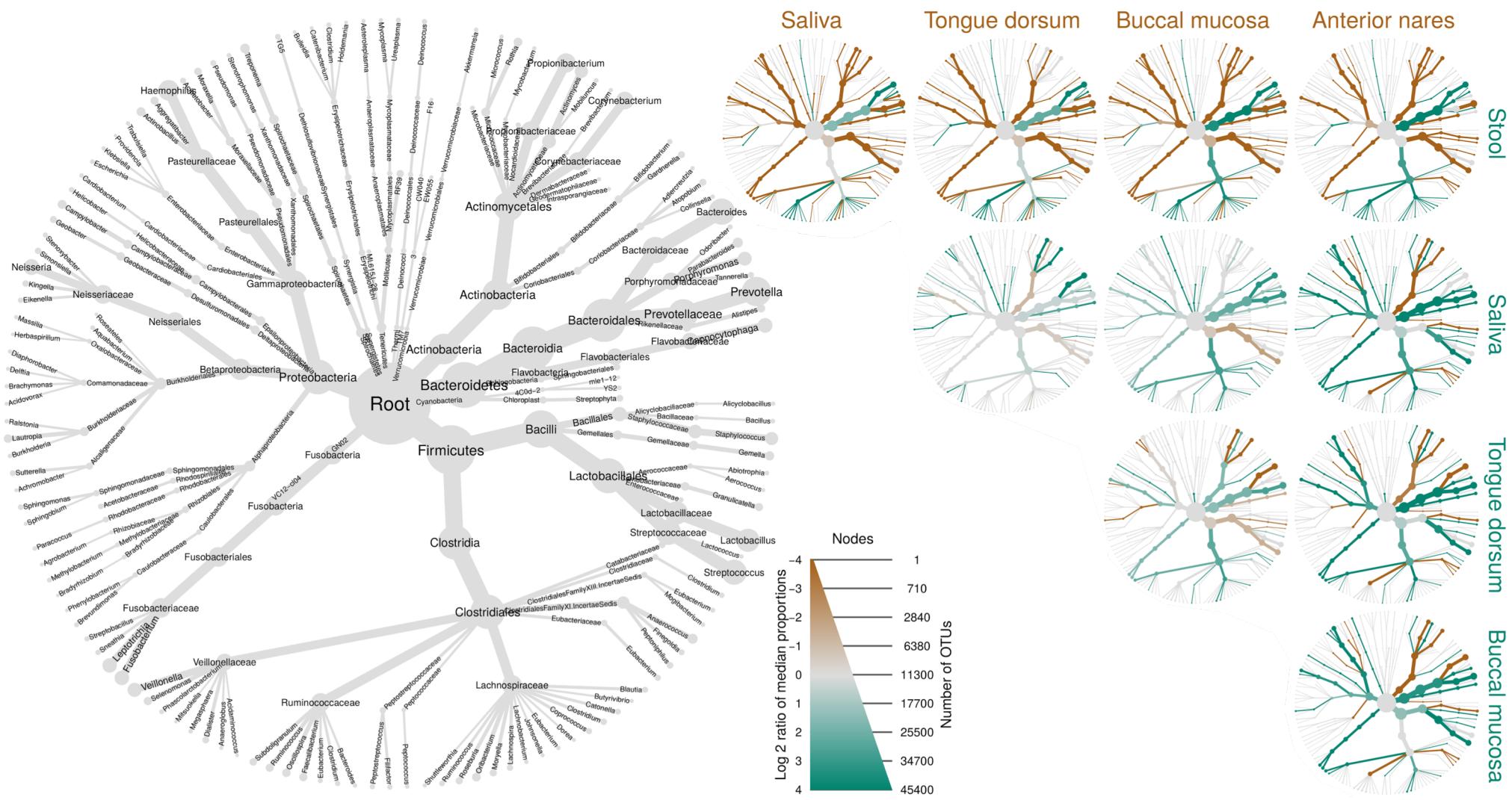
Metacoder: An R package for visualization and manipulation of community taxonomic diversity data

- Stacked bar/pie charts commonly used to plot community composition
- Color representing taxa limits number of taxa that can be plotted
- Heat trees use color and size of nodes and edges to plot up to 4 statistics
- Heat trees allow for the display of more taxa, ranks, and statistics than stacked barcharts



Application example: The Human Microbiome Project

- Heat trees can be used to construct information-dense visualizations
- The plot below shows significant abundance differences between body sites (Wilcoxon rank-sum with false discovery rate correction)



Conlcusions: Areas of collaboration

- Population genomics
 - SSR genotyping
 - GBS
 - HiSeq resequencning and variant calling
- Metabarcdoing
 - Rps10 locus
- Computational tools